#13

1647

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/170,042A

DATE: 03/16/2001
TIME: 16:00:57

P.S

Input Set : D:\PF226D1.txt
Output Set: N:\CRF3\03162001\I170042A.raw

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 3 <110> APPLICANT: Hastings, Gregg
 4        Dillon, Patrick
 6 <120> TITLE OF INVENTION: Human Neuronal Attachment Factor-1
 8 <130> FILE REFERENCE: PF226D1
10 <140> CURRENT APPLICATION NUMBER: 09/170,042A
11 <141> CURRENT FILING DATE: 1998-10-13
13 <160> NUMBER OF SEQ ID NOS: 19
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1105
19 <212> TYPE: DNA
20 <213> ORGANISM: homo sapiens
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (19)..(1011)
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27 cgctgctcct gccgggtg atg gaa aac ccc agc ccg gcc gcc gcc ctg ggc      51
28                    Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly
29                     1               5                  10
31 aag gcc ctc tgc gct ctc ctc ctg gcc act ctc ggc gcc gcc ggc cag      99
32 Lys Ala Leu Cys Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln
33         15                  20                  25
35 cct ctt ggg gga gag tcc atc tgt tcc gcc aga gcc ctg gcc aaa tac     147
36 Pro Leu Gly Gly Glu Ser Ile Cys Ser Ala Arg Ala Leu Ala Lys Tyr
37         30                  35                  40
39 agc atc acc ttc acg ggc aag tgg agc cag acg gcc ttc ccc aag cag     195
40 Ser Ile Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln
41     45                  50                  55
43 tac ccc ctg ttc cgc ccc cct gcc cag tgg tct tcg ctg ctg ggg gcc     243
44 Tyr Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala
45 60                  65                  70                  75
47 gcg cat agc tcc gac tac agc atg tgg agg aag aac cag tac gtc agt     291
48 Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser
49                 80                  85                  90
51 aac ggg ctg cgc gac ttt gcg gag cgc ggc gag gcc tgg gcg ctg atg     339
52 Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met
53         95                 100                 105
55 aag gag atc gag gcg gcg ggg gag gcg ctg cag agc gtg cac gcg gtg     387
56 Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val His Ala Val
57        110                 115                 120
59 ttt tcg gcg ccc gcc gtc ccc agc ggc acc ggg cag acg tcg gcg gag     435
60 Phe Ser Ala Pro Ala Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu
61     125                 130                 135
63 ctg gag gtg cag cgc agg cac tcg ctg gtc tcg ttt gtg gtg cgc atc     483
64 Leu Glu Val Gln Arg Arg His Ser Leu Val Ser Phe Val Val Arg Ile
65 140                 145                 150                 155
67 gtg ccc agc ccc gac tgg ttc gtg ggc gtg gac agc ctg gac ctg tgc     531
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 68 Val Pro Ser Pro Asp Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys
 69                 160                 165                 170
 71 gac ggg gac cgt tgg cgg gaa cag gcg gcg ctg gac ctg tac ccc tac     579
 72 Asp Gly Asp Arg Trp Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr
 73                 175                 180                 185
 75 gac gcc ggg acg gac agc ggc ttc acc ttc tcc tcc ccc aac ttc gcc     627
 76 Asp Ala Gly Thr Asp Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala
 77                 190                 195                 200
 79 acc atc ccg cag gac acg gtg acc gag ata acg tcc tcc tct ccc agc     675
 80 Thr Ile Pro Gln Asp Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser
 81     205                 210                 215
 83 cac ccg gcc aac tcc ttc tac tac ccg cgg ctg aag gcc ctg cct ccc     723
 84 His Pro Ala Asn Ser Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro
 85 220                 225                 230                 235
 87 atc gcc agg gtg aca ctg gtg cgg ctg cga cag agc ccc agg gcc ttc     771
 88 Ile Ala Arg Val Thr Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe
 89                 240                 245                 250
 91 atc cct ccc gcc cca gtc ctg ccc agc agg gac aat gag att gta gac     819
 92 Ile Pro Pro Ala Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp
 93             255                 260                 265
 95 agc gcc tca gtt cca gaa acg ccg ctg gac tgc gag gtc tcc ctg tgg     867
 96 Ser Ala Ser Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp
 97     270                 275                 280
 99 tcg tcc tgg gga ctg tgc gga ggc cac tgt ggg agg ctc ggg acc aag     915
100 Ser Ser Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys
101     285                 290                 295
103 agc agg act cgc tac gtc cgg gtc cag ccc gcc aac aac ggg agc ccc     963
104 Ser Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro
105 300                 305                 310                 315
107 tgc ccc gag ctc gaa gaa gag gct gag tgc gtc cct gat aac tgc gtc    1011
108 Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val
109                 320                 325                 330
111 taagaccaga gccccgcagc ccctggggcc ccccggagcc atggggtgtc gggggctcct  1071
113 gtgcaggctc atgctgcagg cggccgaggg caca                              1105
116 <210> SEQ ID NO: 2
117 <211> LENGTH: 331
118 <212> TYPE: PRT
119 <213> ORGANISM: homo sapiens
121 <400> SEQUENCE: 2
123 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys Ala
124 1               5                   10                  15
127 Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly Gly Glu
128             20                  25                  30
131 Ser Ile Cys Ser Ala Arg Ala Leu Ala Lys Tyr Ser Ile Thr Phe Thr
132         35                  40                  45
135 Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg
136     50                  55                  60
139 Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp
140 65                  70                  75                  80
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143 Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp
144                   85                  90              Met Lys Glu Ile 95
147 Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala
148                  100                 105             110
151 Ala Gly Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala
152         115                 120                 125
155 Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg
156     130                 135                 140
159 Arg His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp
160 145                 150                 155                 160
163 Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp
164                 165                 170                 175
167 Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp
168                 180                 185                 190
171 Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp
172                 195                 200                 205
175 Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser
176     210                 215                 220
179 Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr
180 225                 230                 235                 240
183 Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro
184                 245                 250                 255
187 Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro
188                 260                 265                 270
191 Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu
192                 275                 280                 285
195 Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr
196     290                 295                 300
199 Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu
200 305                 310                 315                 320
203 Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val
204                 325                 330
207 <210> SEQ ID NO: 3
208 <211> LENGTH: 36
209 <212> TYPE: DNA
210 <213> ORGANISM: oligonucleotide
212 <220> FEATURE:
213 <221> NAME/KEY: primer_bind
214 <222> LOCATION: (1)..(36)
215 <223> OTHER INFORMATION: 5' primer containing a BamHI restriction enzyme site followed by
216        21 nucleotides of NAD-1 coding sequence.
219 <400> SEQUENCE: 3                                                      36
220 gccatacggg atccccagcc tcttggggga gagtcc
223 <210> SEQ ID NO: 4
224 <211> LENGTH: 35
225 <212> TYPE: DNA
226 <213> ORGANISM: oligonucleotide
228 <220> FEATURE:
229 <221> NAME/KEY: primer_bind
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230 <222> LOCATION: (1)..(35)
231 <223> OTHER INFORMATION: 3' primer containing complementary sequence to an XbaI site
232        followed by 21 nucleotides of NAF-1 sequence.
235 <400> SEQUENCE: 4                                                              35
236 ggcatacgtc tagattagac gcagttatca gggac
239 <210> SEQ ID NO: 5
240 <211> LENGTH: 41
241 <212> TYPE: DNA
242 <213> ORGANISM: oligonucleotide
244 <220> FEATURE:
245 <221> NAME/KEY: primer_bind
246 <222> LOCATION: (1)..(41).
247 <223> OTHER INFORMATION: 5' primer containing a BamHI restriction enzyme site followed by
248        8 nucleotides resembling an efficient signal for initiation of
249        translation in eukaryotic cells followed by 21 nucleotides of
250        NAF-1 sequence.
253 <400> SEQUENCE: 5                                                              41
254 gccatacggg atccgccatc atggaaaacc ccagcccggc c
257 <210> SEQ ID NO: 6
258 <211> LENGTH: 35
259 <212> TYPE: DNA
260 <213> ORGANISM: oligonucleotide
262 <220> FEATURE:
263 <221> NAME/KEY: primer_bind
264 <222> LOCATION: (1)..(35)
265 <223> OTHER INFORMATION: 3' primer containing the cleavage site for XbaI restriction
266        endonuclease and 21 nucleotides complementary to the
267        3' end of the translated sequence of the NAF-1 gene.
270 <400> SEQUENCE: 6                                                              35
271 ggcatacgtc tagattagac gcagttatca gggac
274 <210> SEQ ID NO: 7
275 <211> LENGTH: 392
276 <212> TYPE: PRT
277 <213> ORGANISM: rat
279 <400> SEQUENCE: 7
281 Pro Thr Gly Thr Gly Cys Val Ile Leu Lys Ala Ser Ile Val Gln Lys
282 1                   5                   10                  15
284 Arg Ile Ile Tyr Phe Gln Asp Glu Gly Ser Leu Thr Lys Lys Leu Cys
285               20                  25                  30
287 Glu Gln Asp Pro Thr Leu Asp Gly Val Thr Asp Arg Pro Ile Leu Asp
288           35                  40                  45
290 Cys Cys Ala Cys Gly Thr Ala Lys Tyr Arg Leu Thr Phe Tyr Gly Asn
291     50                  55                  60
293 Trp Ser Glu Lys Thr His Pro Lys Asp Tyr Pro Arg Arg Ala Asn His
294 65                  70                  75                  80
296 Trp Ser Ala Ile Ile Gly Gly Ser His Ser Lys Asn Tyr Val Leu Trp
297               85                  90                  95
299 Glu Tyr Gly Gly Tyr Ala Ser Glu Gly Val Lys Gln Val Ala Glu Leu
300               100                 105                 110
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302 Gly Ser Pro Val Lys Met Glu Glu Glu Ile Arg Gln Gln Ser Asp Glu
303         115                 120                 125
305 Val Leu Thr Val Ile Lys Ala Lys Ala Gln Trp Pro Ser Trp Gln Pro
306         130                 135                 140
308 Val Asn Val Arg Ala Ala Pro Ser Ala Glu Phe Ser Val Asp Arg Thr
309 145                 150                 155                 160
311 Arg His Leu Met Ser Phe Leu Thr Met Met Gly Pro Ser Pro Asp Trp
312                 165                 170                 175
314 Asn Val Gly Leu Ser Ala Glu Asp Leu Cys Thr Lys Glu Cys Gly Trp
315                 180                 185                 190
317 Val Gln Lys Val Val Gln Asp Leu Ile Pro Trp Asp Ala Gly Thr Asp
318             195                 200                 205
320 Ser Gly Val Thr Tyr Glu Ser Pro Asn Lys Pro Thr Ile Pro Gln Glu
321     210                 215                 220
323 Lys Ile Arg Pro Leu Thr Ser Leu Asp His Pro Gln Ser Pro Phe Tyr
324 225             230                 235                 240
326 Asp Pro Glu Gly Gly Ser Ile Thr Gln Val Ala Arg Val Val Ile Glu
327                 245                 250                 255
329 Arg Ile Ala Arg Lys Gly Glu Gln Cys Asn Ile Val Pro Asp Asn Val
330             260                 265                 270
332 Asp Asp Ile Val Ala Asp Leu Ala Pro Glu Glu Lys Asp Glu Asp Asp
333             275                 280                 285
335 Thr Pro Glu Thr Cys Ile Tyr Ser Asn Trp Ser Pro Trp Ser Ala Cys
336     290                 295                 300
338 Ser Ser Ser Thr Cys Glu Lys Gly Lys Arg Met Arg Gln Arg Met Leu
339 305                 310                 315                 320
341 Lys Ala Gln Leu Asp Leu Ser Val Pro Cys Pro Asp Thr Gln Asp Phe
342                 325                 330                 335
344 Gln Pro Cys Met Gly Pro Gly Cys Ser Asp Glu Asp Gly Ser Thr Cys
345             340                 345                 350
347 Thr Met Ser Glu Trp Ile Thr Trp Ser Pro Cys Ser Val Ser Cys Gly
348             355                 360                 365
350 Met Gly Met Arg Ser Arg Glu Arg Tyr Val Lys Gln Phe Pro Glu Asp
351     370                 375                 380
353 Gly Ser Val Cys Met Leu Pro Thr
354 385                 390
356 <210> SEQ ID NO: 8
357 <211> LENGTH: 52
358 <212> TYPE: PRT
359 <213> ORGANISM: rat
361 <400> SEQUENCE: 8
363 Cys Ile Tyr Ser Asn Trp Ser Pro Trp Ser Ala Cys Ser Ser Ser Thr
364 1               5               10                  15
366 Cys Glu Lys Gly Lys Arg Met Arg Gln Arg Met Leu Lys Ala Gln Leu
367             20                  25                  30
369 Asp Leu Ser Val Pro Cys Pro Asp Thr Gln Asp Phe Gln Pro Cys Met
370         35                  40                  45
372 Gly Pro Gly Cys
373         50
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3/16/01

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/170,042A

DATE: 03/16/2001
TIME: 16:00:58

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Output Set: N:\CRF3\03162001\I170042A.raw

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L:495 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:
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L:679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:901 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:905 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:911 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18